

P2.145: Learning from Tumor Maps and Tissue Microenvironment: New AI-based Approach to Prognostic Risk Profiling in Lung Adenocarcinoma

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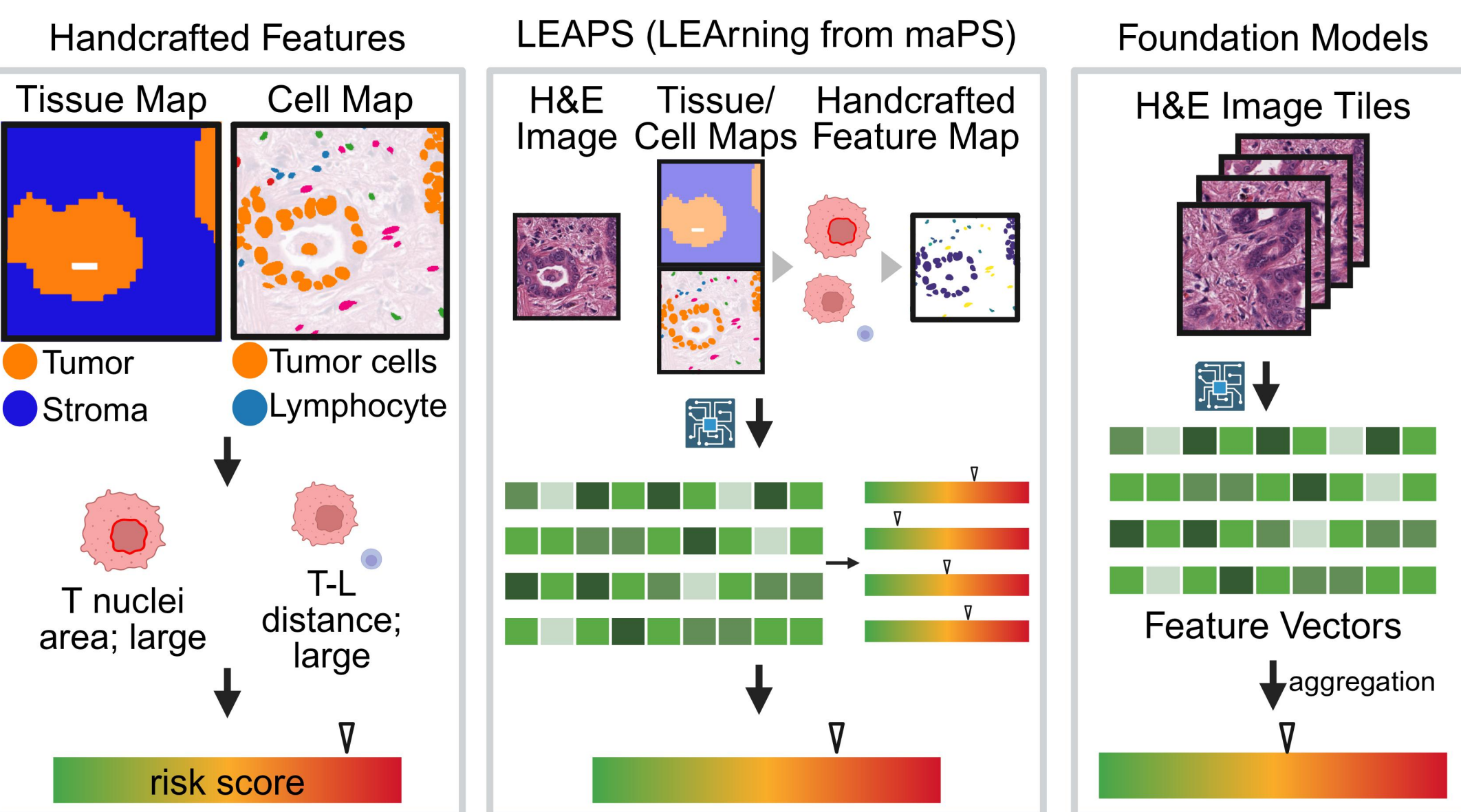
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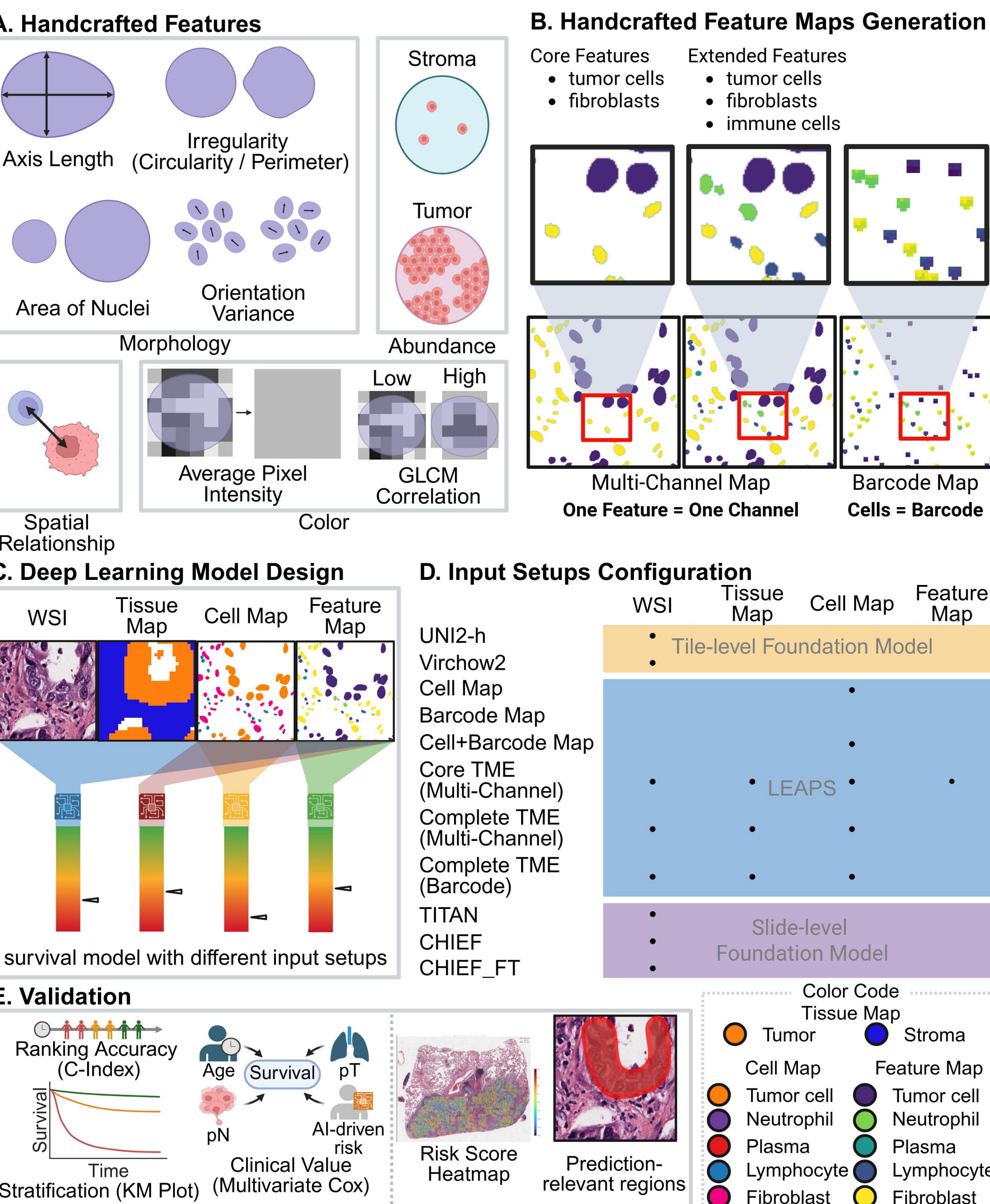
INTRODUCTION

- LUAD shows ITH, reflected in tumor morphology and TME.
- Existing approaches leave a gap between biological explainability and the ability to capture complex morphological patterns.
- The aim of this study is to validate a new framework for interpretable region-level prognostic risk profiling.



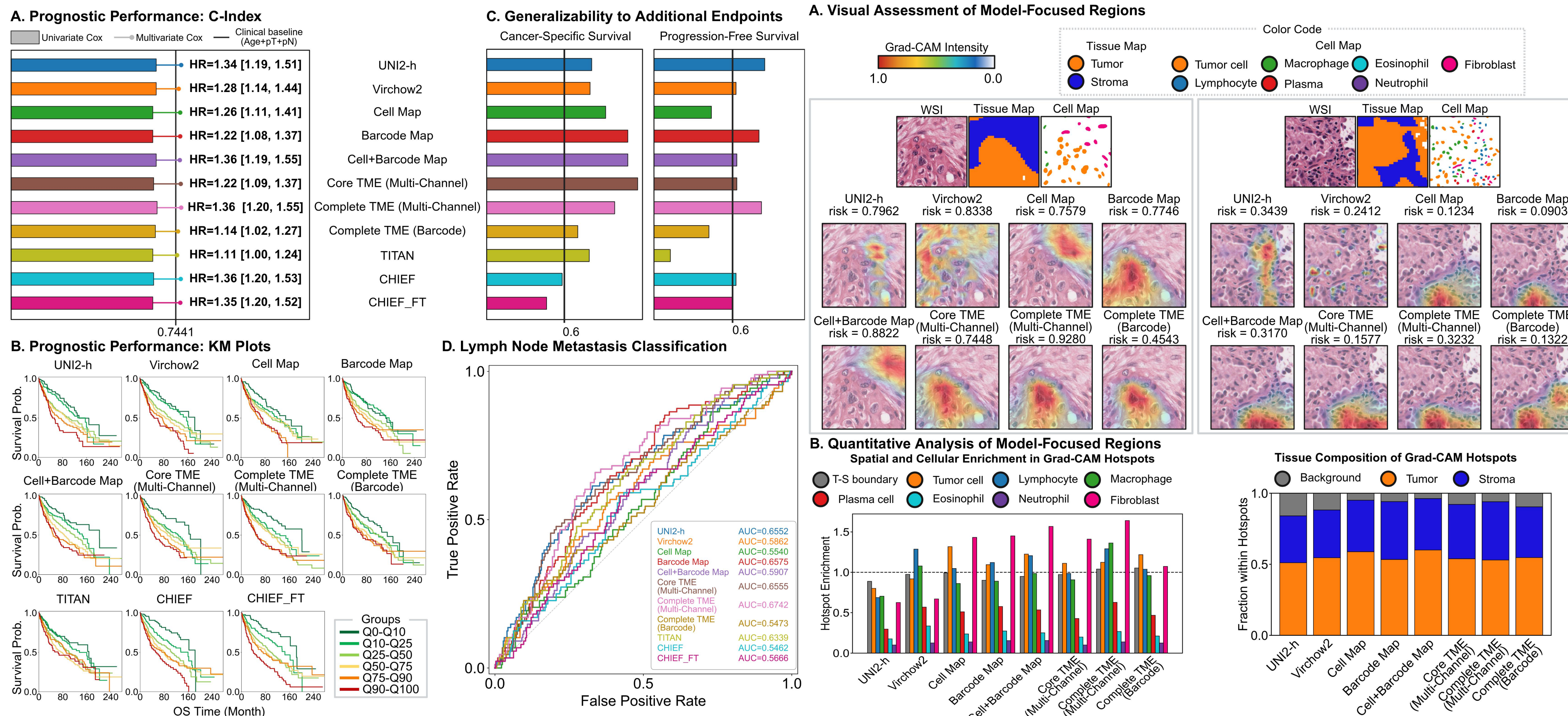
METHODS

- LEAPS (LEARNING from maPS) framework uses deep learning to estimate region-level risks from structured tumor and TME maps.
- Models were developed using TCGA-LUAD (n=245) and externally validated in seven cohorts (n=1,236).
- Overall survival was the primary endpoint.

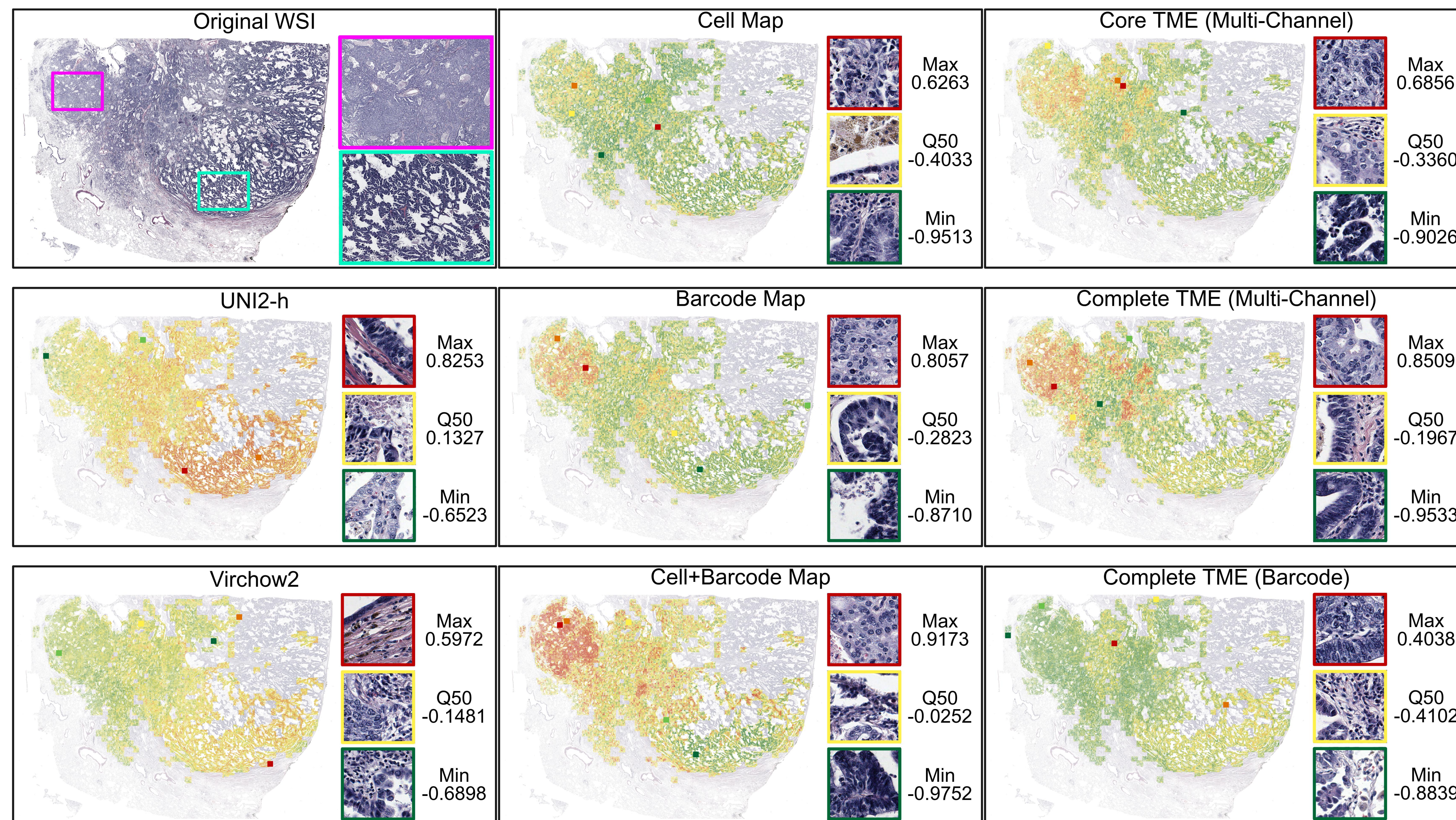


RESULTS

- LEAPS framework captures patient-level prognostic signals and shows broad clinical applicability.
- LEAPS framework identifies plausible risk hotspots within tissue compartments and cellular contexts.



- LEAPS framework reveals risk patterns corresponding to tumor morphology.



DISCUSSION AND CONCLUSION

Summary

- LEAPS bridges handcrafted feature-based and foundation model-based prognosis prediction by applying deep learning to explainable tumor maps.
- LEAPS framework captures patient-level prognostic signals.
- Region-level risk profiles linked predictions to tumor biology, such as tumor morphology, immune cell enrichment, and TME organization.
- Interpretability of LEAPS is supported by spatially structured inputs that preserve tumor and TME context.
- These findings support LEAPS as a practical alternative to conventional black-box models by linking prognostic prediction to interpretable biological features.

Future Directions

- Input-aware integration of H&E morphology and map-derived information
- Detailed cellular phenotyping
- Integration of molecular information

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